

## **RAW SEQUENCE LISTING**

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Application Serial Number: 10597373

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<110> APPLICANT: CASE WESTERN RESERVE UNIVERSITY  
<120> TITLE OF INVENTION: HYBRID AND CHIMERIC POLYPEPTIDES THAT REGULATE ACTIVATION OF COMPLEMENT  
<130> FILE REFERENCE: 200512.00002

<140> CURRENT APPLICATION NUMBER: 10597373  
<141> CURRENT FILING DATE: 0001-01-01  
<150> PRIOR APPLICATION NUMBER: PCT/IB05/50257  
<151> PRIOR FILING DATE: 2005-01-21  
<150> PRIOR APPLICATION NUMBER: 60/537,860  
<151> PRIOR FILING DATE: 2004-01-21  
<160> NUMBER OF SEQ ID NOS: 35  
<170> SOFTWARE: PatentIn Ver. 3.3

<210> SEQ ID NO 1

<211> LENGTH: 381

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 1

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20 25 30  
Trp Gly Asp Cys Gly Leu Pro Pro Asp Val Pro Asn Ala Gln Pro Ala  
35 40 45  
Leu Glu Gly Arg Thr Ser Phe Pro Glu Asp Thr Val Ile Thr Tyr Lys  
50 55 60  
Cys Glu Glu Ser Phe Val Lys Ile Pro Gly Glu Lys Asp Ser Val Ile  
65 70 75 80  
Cys Leu Lys Gly Ser Gln Trp Ser Asp Ile Glu Glu Phe Cys Asn Arg  
85 90 95  
Ser Cys Glu Val Pro Thr Arg Leu Asn Ser Ala Ser Leu Lys Gln Pro  
100 105 110  
Tyr Ile Thr Gln Asn Tyr Phe Pro Val Gly Thr Val Val Glu Tyr Glu  
115 120 125  
Cys Arg Pro Gly Tyr Arg Arg Glu Pro Ser Leu Ser Pro Lys Leu Thr  
130 135 140  
Cys Leu Gln Asn Leu Lys Trp Ser Thr Ala Val Glu Phe Cys Lys Lys  
145 150 155 160  
Lys Ser Cys Pro Asn Pro Gly Glu Ile Arg Asn Gly Gln Ile Asp Val  
165 170 175  
Pro Gly Gly Ile Leu Phe Gly Ala Thr Ile Ser Phe Ser Cys Asn Thr  
180 185 190  
Gly Tyr Lys Leu Phe Gly Ser Thr Ser Ser Phe Cys Leu Ile Ser Gly  
195 200 205  
Ser Ser Val Gln Trp Ser Asp Pro Leu Pro Glu Cys Arg Glu Ile Tyr  
210 215 220  
Cys Pro Ala Pro Pro Gln Ile Asp Asn Gly Ile Ile Gln Gly Glu Arg  
225 230 235 240  
Asp His Tyr Gly Tyr Arg Gln Ser Val Thr Tyr Ala Cys Asn Lys Gly  
245 250 255  
Phe Thr Met Ile Gly Glu His Ser Ile Tyr Cys Thr Val Asn Asn Asp  
260 265 270  
Glu Gly Glu Trp Ser Gly Pro Pro Pro Glu Cys Arg Gly Lys Ser Leu  
275 280 285  
Thr Ser Lys Val Pro Pro Thr Val Gln Lys Pro Thr Thr Val Asn Val  
290 295 300  
Pro Thr Thr Glu Val Ser Pro Thr Ser Gln Lys Thr Thr Thr Lys Thr  
305 310 315 320  
Thr Thr Pro Asn Ala Gln Ala Thr Arg Ser Thr Pro Val Ser Arg Thr  
325 330 335

Thr	Lys	His	Phe	His	Glu	Thr	Thr	Pro	Asn	Lys	Gly	Ser	Gly	Thr	Thr
			340					345						350	
Ser	Gly	Thr	Thr	Arg	Leu	Leu	Ser	Gly	His	Thr	Cys	Phe	Thr	Leu	Thr
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Gly	Leu	Leu	Gly	Thr	Leu	Val	Thr	Met	Gly	Leu	Leu	Thr			
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 <211> LENGTH: 2102  
 <212> TYPE: DNA  
 <213> ORGANISM: Homo sapiens  
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 180 ccccagatgt acctaattgcc cagccagctt tggaggccg tacaagttt cccgaggata  
 240 ctgttaataac gtacaaatgt gaagaaagct ttgtgaaaat tcctggcgag aaggactcag  
 300 ttagtctgcct taagggcagt caatggtcag atattgaaga gttctgcaat cgtagctgc  
 360 aggtgcacac aaggctaaat tctgcattccc tcaaacagcc ttatatact cagaattatt  
 420 ttccagtcgg tactgttgta gaatatgagt gccgtccagg ttacagaaga gaaccttctc  
 480 tatcacaaaa actaacttgc cttcagaatt taaaatggtc cacagcagtc gaattttgta  
 540 aaaagaaaatc atgccttaat ccgggagaaaa tacgaaatgg tcagattgat gtaccaggt  
 600 gcatattatt tggtgcaacc atctccttct catgtAACAC agggtacaaa ttatggct  
 660 cgacttctag ttttgcctt atttcaggca gctctgtcca gtggagtgac ccgttgc  
 720 agtgcagaga aatttattgt ccagcaccac cacaattga caatgaaata attcaagg  
 780 aacgtgacca ttatggat agacagtctg taacgtatgc atgtataaaa ggattcacca  
 840 tgattggaga gcactctatt tattgtactg tgaataatga tgaaggagag tggagtggcc  
 900 caccacctga atgcagagga aaatctctaa cttccaagggt cccaccaaca gttcagaaac  
 960 ctaccacagt aaatgttcca actacagaag tctcaccaac ttctcagaaaa accaccacaa  
 1020 aaaccaccac accaaatgct caagcaacac ggagtacacc tgttccagg acaaccaagc  
 1080 attttcatga aacaacccca aataaaggaa gtggaaaccac ttcaggtact acccgtcttc  
 1140 tatctggca cacgtgtttc acgttgacag gtttgcttgg gacgctagta accatggct  
 1200 tgctgactta gccaaagaag agttaagaag aaaatacaca caagtataca gactgttct  
 1260 agtttcttag acttatctgc atattggata aaataaatgc aattgtgctc ttcatttagg  
 1320 atgctttcat tgtctttaag atgtgttagg aatgtcaaca gagcaaggag aaaaaaggca  
 1380 gtcctggaat cacattctta gcacacccac acctcttggaa aatagaacaa cttgcagaat  
 1440 tgagagtgtat tccttccta aaagtgtaaag aaagcataga gatttgc tatttagat

1500 gggatcacga ggaaaagaga aggaaagtga ttttttcca caagatctgt aatgttattt  
1560 ccacttataa aggaaataaa aaatgaaaaaa cattatttgg atatcaaaag caaataaaaa  
1620 cccaaattcag tctcttctaa gcaaaattgc taaagagaga tgaaccacat tataaagtaa  
1680 tctttggctg taaggcattt tcatacatttcc ttccgggttgg caaaatattt taaaggtaaa  
1740 acatgctggc gaaccagggg tggtgatggc gataagggag gaatataaaaa tgaaagactg  
1800 aatcttcctt tggcacaat atagagtttgc gaaaaaggcct gtgaaagggtg tcttcatttgc  
1860 cttaatgtct taaaaagtat ccagagatac tacaatatta acataagaaaa agattatata  
1920 ttatattctga atcgagatgt ccatagtcaa atttgtaaat cttattctt tgtaatattt  
1980 atttatattt atttatgaca gtgaacattc tgatattaca tgtaaaacaa gaaaagttga  
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2100 gt  
2102

<210> SEQ ID NO 3  
<211> LENGTH: 2044  
<212> TYPE: PRT  
<213> ORGANISM: Homo sapiens  
<400> SEQUENCE: 3  
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Val Gly Pro Pro Ala Pro Gly Leu Pro Phe Cys Cys Gly Gly Ser Leu  
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Leu Ala Val Val Val Leu Leu Ala Leu Pro Val Ala Trp Gly Gln Cys  
35 40 45  
Asn Ala Pro Glu Trp Leu Pro Phe Ala Arg Pro Thr Asn Leu Thr Asp  
50 55 60  
Glu Phe Glu Phe Pro Ile Gly Thr Tyr Leu Asn Tyr Glu Cys Arg Pro  
65 70 75 80  
Gly Tyr Ser Gly Arg Pro Phe Ser Ile Ile Cys Leu Lys Asn Ser Val  
85 90 95  
Trp Thr Gly Ala Lys Asp Arg Cys Arg Arg Lys Ser Cys Arg Asn Pro  
100 105 110  
Pro Asp Pro Val Asn Gly Met Val His Val Ile Lys Gly Ile Gln Phe  
115 120 125  
Gly Ser Gln Ile Lys Tyr Ser Cys Thr Lys Gly Tyr Arg Leu Ile Gly  
130 135 140  
Ser Ser Ser Ala Thr Cys Ile Ile Ser Gly Asp Thr Val Ile Trp Asp  
145 150 155 160  
Asn Glu Thr Pro Ile Cys Asp Arg Ile Pro Cys Gly Leu Pro Pro Thr  
165 170 175  
Ile Thr Asn Gly Asp Phe Ile Ser Thr Asn Arg Glu Asn Phe His Tyr  
180 185 190  
Gly Ser Val Val Thr Tyr Arg Cys Asn Pro Gly Ser Gly Gly Arg Lys  
195 200 205  
Val Phe Glu Leu Val Gly Glu Pro Ser Ile Tyr Cys Thr Ser Asn Asp  
210 215 220  
Asp Gln Val Gly Ile Trp Ser Gly Pro Ala Pro Gln Cys Ile Ile Pro  
225 230 235 240  
Asn Lys Cys Thr Pro Pro Asn Val Glu Asn Gly Ile Leu Val Ser Asp  
245 250 255

Asn Arg Ser Leu Phe Ser Leu Asn Glu Val Val Glu Phe Arg Cys Gln  
260 265 270  
Pro Gly Phe Val Met Lys Gly Pro Arg Arg Val Lys Cys Gln Ala Leu  
275 280 285  
Asn Lys Trp Glu Pro Glu Leu Pro Ser Cys Ser Arg Val Cys Gln Pro  
290 295 300  
Pro Pro Asp Val Leu His Ala Glu Arg Thr Gln Arg Asp Lys Asp Asn  
305 310 315 320  
Phe Ser Pro Gly Gln Glu Val Phe Tyr Ser Cys Glu Pro Gly Tyr Asp  
325 330 335  
Leu Arg Gly Ala Ala Ser Met Arg Cys Thr Pro Gln Gly Asp Trp Ser  
340 345 350  
Pro Ala Ala Pro Thr Cys Glu Val Lys Ser Cys Asp Asp Phe Met Gly  
355 360 365  
Gln Leu Leu Asn Gly Arg Val Leu Phe Pro Val Asn Leu Gln Leu Gly  
370 375 380  
Ala Lys Val Asp Phe Val Cys Asp Glu Gly Phe Gln Leu Lys Gly Ser  
385 390 395 400  
Ser Ala Ser Tyr Cys Val Leu Ala Gly Met Glu Ser Leu Trp Asn Ser  
405 410 415  
Ser Val Pro Val Cys Glu Gln Ile Phe Cys Pro Ser Pro Pro Val Ile  
420 425 430  
Pro Asn Gly Arg His Thr Gly Lys Pro Leu Glu Val Phe Pro Phe Gly  
435 440 445  
Lys Ala Val Asn Tyr Thr Cys Asp Pro His Pro Asp Arg Gly Thr Ser  
450 455 460  
Phe Asp Leu Ile Gly Glu Ser Thr Ile Arg Cys Thr Ser Asp Pro Gln  
465 470 475 480  
Gly Asn Gly Val Trp Ser Ser Pro Ala Pro Arg Cys Gly Ile Leu Gly  
485 490 495  
His Cys Gln Ala Pro Asp His Phe Leu Phe Ala Lys Leu Lys Thr Gln  
500 505 510  
Thr Asn Ala Ser Asp Phe Pro Ile Gly Thr Ser Leu Lys Tyr Glu Cys  
515 520 525  
Arg Pro Glu Tyr Tyr Gly Arg Pro Phe Ser Ile Thr Cys Leu Asp Asn  
530 535 540  
Leu Val Trp Ser Ser Pro Lys Asp Val Cys Lys Arg Lys Ser Cys Lys  
545 550 555 560  
Thr Pro Pro Asp Pro Val Asn Gly Met Val His Val Ile Thr Asp Ile  
565 570 575  
Gln Val Gly Ser Arg Ile Asn Tyr Ser Cys Thr Thr Gly His Arg Leu  
580 585 590  
Ile Gly His Ser Ser Ala Glu Cys Ile Leu Ser Gly Asn Ala Ala His  
595 600 605  
Trp Ser Thr Lys Pro Pro Ile Cys Gln Arg Ile Pro Cys Gly Leu Pro  
610 615 620  
Pro Thr Ile Ala Asn Gly Asp Phe Ile Ser Thr Asn Arg Glu Asn Phe  
625 630 635 640  
His Tyr Gly Ser Val Val Thr Tyr Arg Cys Asn Pro Gly Ser Gly Gly  
645 650 655  
Arg Lys Val Phe Glu Leu Val Gly Glu Pro Ser Ile Tyr Cys Thr Ser  
660 665 670  
Asn Asp Asp Gln Val Gly Ile Trp Ser Gly Pro Ala Pro Gln Cys Ile  
675 680 685  
Ile Pro Asn Lys Cys Thr Pro Pro Asn Val Glu Asn Gly Ile Leu Val  
690 695 700  
Ser Asp Asn Arg Ser Leu Phe Ser Leu Asn Glu Val Val Glu Phe Arg  
705 710 715 720  
Cys Gln Pro Gly Phe Val Met Lys Gly Pro Arg Arg Val Lys Cys Gln  
725 730 735  
Ala Leu Asn Lys Trp Glu Pro Glu Leu Pro Ser Cys Ser Arg Val Cys

	740	745	750												
Gln	Pro	Pro	Asp	Val	Leu	His	Ala	Glu	Arg	Thr	Gln	Arg	Asp	Lys	
755						760					765				
Asp	Asn	Phe	Ser	Pro	Gly	Gln	Glu	Val	Phe	Tyr	Ser	Cys	Glu	Pro	Gly
770						775				780					
Tyr	Asp	Leu	Arg	Gly	Ala	Ala	Ser	Met	Arg	Cys	Thr	Pro	Gln	Gly	Asp
785						790				795				800	
Trp	Ser	Pro	Ala	Ala	Pro	Thr	Cys	Glu	Val	Lys	Ser	Cys	Asp	Asp	Phe
						805				810				815	
Met	Gly	Gln	Leu	Leu	Asn	Gly	Arg	Val	Leu	Phe	Pro	Val	Asn	Leu	Gln
						820				825				830	
Leu	Gly	Ala	Lys	Val	Asp	Phe	Val	Cys	Asp	Glu	Gly	Phe	Gln	Leu	Lys
						835				840				845	
Gly	Ser	Ser	Ala	Ser	Tyr	Cys	Val	Leu	Ala	Gly	Met	Glu	Ser	Leu	Trp
						850				855				860	
Asn	Ser	Ser	Val	Pro	Val	Cys	Glu	Gln	Ile	Phe	Cys	Pro	Ser	Pro	Pro
						865				870				880	
Val	Ile	Pro	Asn	Gly	Arg	His	Thr	Gly	Lys	Pro	Leu	Glu	Val	Phe	Pro
						885				890				895	
Phe	Gly	Lys	Ala	Val	Asn	Tyr	Thr	Cys	Asp	Pro	His	Pro	Asp	Arg	Gly
						900				905				910	
Thr	Ser	Phe	Asp	Leu	Ile	Gly	Glu	Ser	Thr	Ile	Arg	Cys	Thr	Ser	Asp
						915				920				925	
Pro	Gln	Gly	Asn	Gly	Val	Trp	Ser	Ser	Pro	Ala	Pro	Arg	Cys	Gly	Ile
						930				935				940	
Leu	Gly	His	Cys	Gln	Ala	Pro	Asp	His	Phe	Leu	Phe	Ala	Lys	Leu	Lys
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Thr	Gln	Thr	Asn	Ala	Ser	Asp	Phe	Pro	Ile	Gly	Thr	Ser	Leu	Lys	Tyr
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Glu	Cys	Arg	Pro	Glu	Tyr	Tyr	Gly	Arg	Pro	Phe	Ser	Ile	Thr	Cys	Leu
						980				985				990	
Asp	Asn	Leu	Val	Trp	Ser	Ser	Pro	Lys	Asp	Val	Cys	Lys	Arg	Lys	Ser
						995				1000				1005	
Cys	Lys	Thr	Pro	Pro	Asp	Pro	Val	Asn	Gly	Met	Val	His	Val	Ile	Thr
						1010				1015				1020	
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						1025				1030				1040	
Arg	Leu	Ile	Gly	His	Ser	Ser	Ala	Glu	Cys	Ile	Leu	Ser	Gly	Asn	Thr
						1045				1050				1055	
Ala	His	Trp	Ser	Thr	Lys	Pro	Pro	Ile	Cys	Gln	Arg	Ile	Pro	Cys	Gly
						1060				1065				1070	
Leu	Pro	Pro	Thr	Ile	Ala	Asn	Gly	Asp	Phe	Ile	Ser	Thr	Asn	Arg	Glu
						1075				1080				1085	
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						1090				1095				1100	
Arg	Gly	Arg	Lys	Val	Phe	Glu	Leu	Val	Gly	Glu	Pro	Ser	Ile	Tyr	Cys
						1105				1110				1120	
Thr	Ser	Asn	Asp	Asp	Gln	Val	Gly	Ile	Trp	Ser	Gly	Pro	Ala	Pro	Gln
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Cys	Ile	Ile	Pro	Asn	Lys	Cys	Thr	Pro	Pro	Asn	Val	Glu	Asn	Gly	Ile
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Leu	Val	Ser	Asp	Asn	Arg	Ser	Leu	Phe	Ser	Leu	Asn	Glu	Val	Val	Glu
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Phe	Arg	Cys	Gln	Pro	Gly	Phe	Val	Met	Lys	Gly	Pro	Arg	Arg	Val	Lys
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Cys	Gln	Ala	Leu	Asn	Lys	Trp	Glu	Pro	Glu	Leu	Pro	Ser	Cys	Ser	Arg
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Val	Cys	Gln	Pro	Pro	Pro	Glu	Ile	Leu	His	Gly	Glu	His	Thr	Pro	Ser
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